

LISTING OF CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application:

1-62. (Canceled).

63. (Currently amended) A method to identify a compound that modulates chromatin remodeling of a specific DNA sequence within chromatin comprising:

a) providing chromatin assembled DNA containing a specific DNA sequence, which specific DNA sequence comprises a binding site for a zinc finger DNA binding domain peptide of a nucleic acid regulatory protein, which zinc finger DNA binding domain peptide ~~immunoprecipitates~~interacts directly with a SWI/SNF chromatin remodeling complex comprising BRG1;

b) contacting the chromatin assembled DNA with:

- 1) the SWI/SNF chromatin remodeling complex comprising BRG1, and
- 2) the zinc finger DNA binding domain peptide of the nucleic acid regulatory

protein;

under conditions that permit the direct interaction of the SWI/SNF chromatin remodeling complex and the zinc finger DNA binding domain peptide; and

c) determining the level of chromatin remodeling in the presence and absence of a test compound; wherein a difference in the level of chromatin remodeling in the presence and absence of the test compound identifies the test compound as a compound that modulates chromatin remodeling of the specific DNA sequence within chromatin.

64. (Previously presented) The method of claim 63, wherein the specific DNA sequence is an individual gene or portion thereof, a regulatory region or a chromosomal region.

65. (Canceled).

66. **(Previously presented)** The method of claim 63, wherein the nucleic acid regulatory protein is a transcription factor.

67-71. **(Canceled).**

72. **(Previously presented)** The method of claim 63, wherein the SWI/SNF chromatin remodeling complex is E-RC1.

73. **(Canceled).**

74. **(Currently amended)** The method of claim 63, wherein the SWI/SNF chromatin remodeling complex is a minimal SWI/SNF complex consisting of BRG1 and BAF155.

75-79. **(Canceled).**

80. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from GATA-1, Spl, EKLF, FKLf, BKLf, GKLF, LKLf, Wilm's tumor suppressor protein (WT1), BRCA1, BRCA2, KRAB, BTB/POZ, Zif268, GLI, Xfin, a BTB/POZ domain containing zinc finger protein, PLZF (promyelocytic leukemia zinc finger), or a nuclear hormone receptor.

81. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from a nuclear hormone receptor.

82. **(Previously presented)** The method of claim 81, wherein the nuclear hormone receptor is selected from the group consisting of an androgen, estrogen, thyroid, progesterone, and glucocorticoid receptor.

83. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide binds to a promoter, an enhancer, an insulator, a silencer, or locus of control regions (LCRs).

84. **(Previously presented)** The method of claim 63, wherein the test compound is a small molecule.

85. **(Previously presented)** The method of claim 63, wherein the test compound is a peptide.

86-87. **(Canceled).**

88. **(Previously presented)** The method of claim 63, wherein the amount of chromatin remodeling is determined by assaying for DNase hypersensitive sites within the specific DNA sequence.

89-102. **(Canceled).**

103. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from GATA-1, Spl, or EKLF.

104. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from GATA-1 or EKLF.

105. **(Previously presented)** The method of claim 63, wherein the zinc finger DNA binding domain peptide is from EKLF.

106. **(New)** The method of claim 63, wherein the SWI/SNF chromatin remodeling complex is a minimal SWI/SNF complex consisting of BRG1 and BAF155; and wherein the zinc finger DNA binding domain peptide is from GATA-1, Spl, or EKLF.